

Supplementary Table S1. Epidemiological data of all isolates characterized in this study by whole-genome sequencing. Phylogenetic group 1: ancestral *S. sciuri* background; phylogenetic group 2: *S. sciuri sciuri*; phylogenetic group 3: *S. sciuri* new subspecies; phylogenetic group 4: *S. sciuri rodentius*; phylogenetic group 5: *S. sciuri carnicum*.

Strain	Species (<i>S. sciuri</i> phylogenetic group)	MIC (µg/ml)	Year of isolation	Origin	Geographic location	Source or Reference
402567	<i>S. fleurettii</i>	>256	2004	Horse	The Netherlands	E. van Duijkeren
CH19	<i>S. fleurettii</i>	8	2010	Bovine mastitis milk	Switzerland	(1)
CH20	<i>S. fleurettii</i>	6	2010	Bovine mastitis milk	Switzerland	(1)
CH21	<i>S. fleurettii</i>	4	2010	Bovine mastitis milk	Switzerland	(1)
CH22	<i>S. fleurettii</i>	1	2010	Bovine mastitis milk	Switzerland	(1)
CH23	<i>S. fleurettii</i>	4	2010	Bovine mastitis milk	Switzerland	(1)
CH24	<i>S. fleurettii</i>	>256	2010	Bovine mastitis milk	Switzerland	(1)
CH25	<i>S. fleurettii</i>	4	2010	Bovine mastitis milk	Switzerland	(1)
CH26	<i>S. fleurettii</i>	>256	2010	Bovine mastitis milk	Switzerland	(1)
CH27	<i>S. fleurettii</i>	2	2010	Bovine mastitis milk	Switzerland	(1)
CH28	<i>S. fleurettii</i>	1	2010	Bovine mastitis milk	Switzerland	(1)
CH29	<i>S. fleurettii</i>	4	2010	Bovine mastitis milk	Switzerland	(1)
JUG1	<i>S. sciuri</i> (1)	>256	2002	Domestic dog	Czech Republic	I. Sedláček
K22	<i>S. sciuri</i> (1)	1.5	1992	Morgan Horse	USA	(2)
M1886	<i>S. sciuri</i> (1)	64	2011	Human	Denmark	Hvidovre Hospital
K1	<i>S. sciuri</i> (2)	0.75	1972	Eastern grey squirrel	USA	(2)
K105	<i>S. sciuri</i> (2)	1	1971	Human	USA	(2)
K13	<i>S. sciuri</i> (2)	0.5	1992	Eastern grey squirrel	USA	(2)
K139	<i>S. sciuri</i> (2)	1	1992	Holstein cow	USA	(2)
K14	<i>S. sciuri</i> (2)	0.75	1992	Eastern harvest mouse	USA	(2)
K140	<i>S. sciuri</i> (2)	1	1972	Opossum	USA	(2)
K142	<i>S. sciuri</i> (2)	1	1992	Horse	USA	(2)
K143	<i>S. sciuri</i> (2)	1	1972	Racoon	USA	(2)
K144	<i>S. sciuri</i> (2)	1	1992	Jersey calf	USA	(2)
K149	<i>S. sciuri</i> (2)	0.75	1972	Eastern grey squirrel	USA	(2)
K21	<i>S. sciuri</i> (2)	0.5	1993	Pilot whale	USA	(2)
K23	<i>S. sciuri</i> (2)	0.75	1992	Red kangaroo	USA	(2)
K25	<i>S. sciuri</i> (2)	0.5	1992	Prairie vole	USA	(2)
KLO56	<i>S. sciuri</i> (2)	0.75	1972	Opossum	USA	(2)
KLO58	<i>S. sciuri</i> (2)	0.75	1972	Squirrel monkey	USA	(2)
KLO63	<i>S. sciuri</i> (2)	1	1972	Eastern grey squirrel	USA	(2)
KLO64	<i>S. sciuri</i> (2)	2	1972	Southern flying squirrel	USA	(2)
CH17	<i>S. sciuri</i> (3)	>256	2004	Horse	Switzerland	(3)
CH18	<i>S. sciuri</i> (3)	>256	2005	Horse	Switzerland	(3)
D573	<i>S. sciuri</i> (3)	>256	2007	Human	Denmark	Hvidovre Hospital
HSM805	<i>S. sciuri</i> (3)	0.75	2010	Human	Portugal	J. Melo-Cristino
HSM851	<i>S. sciuri</i> (3)	16	2010	Human	Portugal	J. Melo-Cristino
JUG17	<i>S. sciuri</i> (3)	>256	2002	Human	Yugoslavia	I. Sedláček
JUG2	<i>S. sciuri</i> (3)	0.75	2002	Domestic dog	Yugoslavia	I. Sedláček
K132	<i>S. sciuri</i> (3)	0.5	1976	Howler monkey	Panama	(2)
K141	<i>S. sciuri</i> (3)	1	1992	California mouse	USA	(2)
K148	<i>S. sciuri</i> (3)	0.38	1992	Bottlenose dolphin	USA	(2)
K2	<i>S. sciuri</i> (3)	1	1992	Beef tongue	USA	(2)
K20	<i>S. sciuri</i> (3)	1	1992	Bottlenose dolphin	USA	(2)
K24	<i>S. sciuri</i> (3)	0.75	1992	Morgan Horse	USA	(2)
K51	<i>S. sciuri</i> (3)	1.5	1971	Human	USA	(2)
K61	<i>S. sciuri</i> (3)	1.5	1992	Pilot whale	USA	(2)
K69	<i>S. sciuri</i> (3)	1	1986	Human	USA	(2)
KLO59	<i>S. sciuri</i> (3)	2	1972	Domestic dog	USA	(2)
M1234	<i>S. sciuri</i> (3)	>256	2009	Human	Denmark	Hvidovre Hospital

Strain	Species (<i>S. sciuri</i> phylogenetic group)	MIC (µg/ml)	Year of isolation	Origin	Geographic location	Source or Reference
M1640	<i>S. sciuri</i> (3)	96	2010	Human	Denmark	Hvidovre Hospital
M1653	<i>S. sciuri</i> (3)	>256	2010	Human	Denmark	Hvidovre Hospital
M2276	<i>S. sciuri</i> (3)	>256	2011	Human	Denmark	Hvidovre Hospital
M2590	<i>S. sciuri</i> (3)	>256	2012	Human	Denmark	Hvidovre Hospital
M2710	<i>S. sciuri</i> (3)	>256	2012	Human	Denmark	Hvidovre Hospital
M692	<i>S. sciuri</i> (3)	96	2007	Human	Denmark	Hvidovre Hospital
SS16	<i>S. sciuri</i> (3)	0.75	1996	Human	Portugal	(4)
SS18	<i>S. sciuri</i> (3)	0.75	1996	Human	Portugal	(4)
SS23	<i>S. sciuri</i> (3)	1	1997	Human	Portugal	(4)
SS24	<i>S. sciuri</i> (3)	0.75	1997	Human	Portugal	(4)
SS27	<i>S. sciuri</i> (3)	0.75	1998	Human	Portugal	(4)
SS3	<i>S. sciuri</i> (3)	1	1996	Human	Portugal	(4)
SS5	<i>S. sciuri</i> (3)	1	1996	Human	Portugal	(4)
K3	<i>S. sciuri</i> (4)	>256	1992	Neonatal ward	Mozambique	(2)
CH16	<i>S. sciuri</i> (4)	24	2004	Horse	Switzerland	(3)
K10	<i>S. sciuri</i> (4)	0.75	1992	European red squirrel	USA	(2)
K125	<i>S. sciuri</i> (4)	1	1992	Cotton rat	USA	(2)
K27	<i>S. sciuri</i> (4)	0.75	1992	Norway rat	USA	(2)
K29	<i>S. sciuri</i> (4)	0.75	1992	Norway rat	USA	(2)
K4	<i>S. sciuri</i> (4)	>256	1992	Human	Mozambique	(2)
K5	<i>S. sciuri</i> (4)	2	1992	Human	Mozambique	(2)
K6	<i>S. sciuri</i> (4)	>256	1992	Human	Mozambique	(2)
K7	<i>S. sciuri</i> (4)	>256	1992	Human	Mozambique	(2)
K83	<i>S. sciuri</i> (4)	0.75	1992	Human	Czech Republic	(2)
SS34	<i>S. sciuri</i> (4)	0.75	1996	Human	Portugal	(4)
SS37	<i>S. sciuri</i> (4)	25	1996	Human	Portugal	(4)
SS41	<i>S. sciuri</i> (4)	3	1996	Human	Portugal	(4)
11/01	<i>S. sciuri</i> (5)	0.5	2002	Human	Czech Republic	O. Melter
CCUG38359	<i>S. sciuri</i> (5)	0.75	2002	Human	Czech Republic	O. Melter
K11	<i>S. sciuri</i> (5)	0.75	1990	Veal leg	USA	(2)
K116	<i>S. sciuri</i> (5)	0.75	1992	Beef lips	USA	(2)
K12	<i>S. sciuri</i> (5)	1	1992	Arabian Horse	USA	(2)
K16	<i>S. sciuri</i> (5)	0.75	1992	Jersey calf	USA	(2)
K163	<i>S. sciuri</i> (5)	0.75	1992	Holstein cow	USA	(2)
K30	<i>S. sciuri</i> (5)	1.5	1992	Jersey cattle heifer	USA	(2)
K31	<i>S. sciuri</i> (5)	0.5	1992	Jersey cattle calf	USA	(2)
K32	<i>S. sciuri</i> (5)	0.75	1992	Jersey cattle calf	USA	(2)
K33	<i>S. sciuri</i> (5)	0.75	1992	Jersey cattle heifer	USA	(2)
H39	<i>S. vitulinus</i>	0.75	2005	Horse	Denmark	L. Guardabassi P. Damborg
H91	<i>S. vitulinus</i>	2	2005	Horse	Denmark	L. Guardabassi P. Damborg
401946	<i>S. vitulinus</i>	2	2004	Horse	The Netherlands	E. van Duijkeren
CH1	<i>S. vitulinus</i>	1	2005	Horse	Switzerland	(3)
CH2	<i>S. vitulinus</i>	4	2004	Horse	Switzerland	(3)
CH3	<i>S. vitulinus</i>	0.75	2005	Horse	Switzerland	(3)
CH4	<i>S. vitulinus</i>	0.75	2004	Horse	Switzerland	(3)
CH5	<i>S. vitulinus</i>	>256	2005	Horse	Switzerland	(3)
CH6	<i>S. vitulinus</i>	1.5	2004	Horse	Switzerland	(3)
CH7	<i>S. vitulinus</i>	0.75	2004	Horse	Switzerland	(3)
CH8	<i>S. vitulinus</i>	0.19	2005	Horse	Switzerland	(3)
CH9	<i>S. vitulinus</i>	0.5	2004	Horse	Switzerland	(3)
CH10	<i>S. vitulinus</i>	0.5	2004	Horse	Switzerland	(3)
CH11	<i>S. vitulinus</i>	0.5	2005	Horse	Switzerland	(3)
CH12	<i>S. vitulinus</i>	0.5	2004	Horse	Switzerland	(3)

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CH13	<i>S. vitulinus</i>	0.1	2004	Horse	Switzerland	(3)
CH14	<i>S. vitulinus</i>	0.5	2005	Horse	Switzerland	(3)
CH15	<i>S. vitulinus</i>	>256	2004	Horse	Switzerland	(3)

Supplementary Table S2. Content of SCC and SCCmec elements found among *S. sciuri*, *S. vitulinus* and *S. fleurettii*. Only the elements flanked by DR and/or IR repeats are listed on the table.

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
11/01 (<i>S. sciuri</i>)	SCC _{11/01} (53848)	GGGGAAGCGTATCATAAATGATGCGGTTTTT	Threonine dehydrogenase	47225-48262
			Type I restriction modification enzyme	48946-51738
			Type I restriction modification methyltransferase	51850-53406
			Type I restriction modification S subunit	53755-54669
			Hypothetical protein 1: 47.6% KF234240 (SCCmec IVa – J1)	54754-55527
			ORF	55532-56110
			Transcriptional regulator	56407-57099
			Ferroxidase	57116-57667
			Copper chaperone	57669-57905
			Cadmium-transporting ATPase	57969-59819
			ORF	60127-60252
			<i>cadC</i>	60591-60959
			Cadmium-transporting ATPase	60952-63135
			<i>cadD</i>	63233-63460
			Hypothetical protein 2: 96.62% CP006838 (SCCmec III – J2)	63478-63684
			Hypothetical protein 3: 66.9% CP006838 (SCCmec III – J2)	63686-64090
			<i>repB</i>	64320-65000
			Hypothetical protein 4: 76.92% HF569115 (SCCmec IVa+ <i>ccrAB1</i> – J3)	65126-65629
			Hypothetical protein 5: 68.69% AB505628 (SCCmec IX – J3)	65645-65953
			Hypothetical protein 6: 90.69% AB505628 (SCCmec IX – J3)	66038-66391
			<i>ccrB5</i>	66861-68489
			<i>ccrA5</i>	68510-69859
			Hypothetical protein 7: 78.56% AB705452 (SCCmec IX – J2)	70038-71828
			Hypothetical protein 8: 93.36% AB505628 (SCCmec IX – J2)	71954-73384
			ATPase	74084-75607
			<i>copaA</i> – truncated	75629-76147
			Putative lipoprotein	76165-76710

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			ORF	77190-77651
			<i>arsC</i>	78815-79021
			Metallo-βactamase family protein-truncated	81553-81814
			IS257 transposase	88244-88759
			IS431 transposase	88719-88919
			Acyltransferase precursor	91722-92195
			Oxidase	92196-93692
			Glycosyltransferase	93753-94796
			Dehydrosqualene synthase	94852-95733
			Dehydrosqualene desaturase	95730-97235
			General stress protein 26	97284-97709
			Deoxyribodipyrimidine photolyase	97893-99275
			Hypothetical protein 10: 58.69% HE993884 (<i>SCCmec mecC S. xylosus</i> - J1)	99525-99965
K6 (<i>S. sciuri</i>)	SCC _{K6} (15937)	ATGATGCGGTTTTTT	Hypothetical protein 1: 78.81% CP006630 (<i>SCCmec V</i> – J1)	152605-153912
			Hypothetical protein 2: 90.29% CP006838 (<i>SCCmec III</i> – J1)	154412-155461
			ORF	155593-155883
			Putative helicase	155883-157676
			<i>ccrA5</i>	157854-159206
			<i>ccrB</i> new type 2: 72% <i>ccrB1</i>	159223-160854
			Hypothetical protein 3: 95.19% CP006838 (<i>SCCmec III</i> – J2)	161749-162060
			Hypothetical protein 4: 99.8% AB505628 (<i>SCCmec IX</i> – J3)	162081-162584
			Plasmid replication initiation protein	162786-163745
			DNA modification methylase	163595-167209
			Conserved domain protein	167299-168210
K6 (<i>S. sciuri</i>)	ΨSCC _{K6} (10930)	AAAACCGCATCATTT	Permease	168506-168886
			ORF	168962-169546
			Mobile element protein	170153-171040
			TPR domain protein in aerotolerance operon	171224-173869
			ORF	174071-174214

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			Hypothetical protein 1: 54.97% CP006838 (SCCmec III – J3)	174287-174838
			Hypothetical protein 2: 80.65% HE980450 (SCCmec III – J3)	174842-175822
			ORF	176033-176935
			ORF	177041-177358
			Hypothetical protein 3: 65.17% AB373032 (SCCmec 5C1 – J1)	177847-179250
K6 (<i>S. sciuri</i>)	SCCmec III-like structure B (43815)	GATGCGGTTTTTT	Arsenic resistance operon repressor	179490-179804
			ORF	179758-180168
			Arsenic efflux pump	180722-181144
			Arsenate reductase	181162-181563
			Transcriptional regulator	181689-181991
			<i>chrA</i>	182142-183164
			Polysulfide binding protein	183357-184691
			Disulfide bond regulator	184722-185789
			Transcriptional regulator	185927-186187
			Putative transmembrane protein	186208-186942
			Abortive phage resistance protein	187360-188163
			Abi-alpha protein	188176-189339
			ORF	189449-190987
			ORF	191190-191426
			ORF	191428-193215
			Hypothetical protein 1: 72.76% AB705452 (SCCmec IX – J2)	193305-193583
			<i>ccrA3</i>	193772-195118
			<i>ccrB5</i>	195139-196767
			Hypothetical protein 2: 100% JQ412578 (SCCmec II – J2)	197238-197588
			Hypothetical protein 3: 99.68% JQ412578 (SCCmec II – J2)	197673-197984
			Hypothetical protein 4: 100% JQ412578 (SCCmec II – J2)	198003-198524
			Hypothetical protein 5: 99.52% CP006838 (SCCmec III – J2)	198526-198732
			DNA repair protein RadC	198725-199048
			Mobile element protein	199243-201135

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			Mobile element protein	201142-201303
			Mobile element protein	201298-202620
			Mercuric ion reductase	202862-204502
			Mercuric resistance operon regulatory protein	204527-204919
			Cadmium efflux system accessory protein	205631-205996
			Cadmium transporting ATPase	205989-208403
			Cadmium resistance protein	208484-209101
			Hypothetical protein 1: 60.32% CP006838 (SCCmec III – J2)	209369-209998
			Hypothetical protein 2: 100% CP006838 (SCCmec III – J2)	210013-210273
			Disulfide bond regulator	210409-211473
			Zn-dependent hydroacylglutathione hydrolase	211503-212444
			Polysulfide binding protein	212535-212840
			Transcriptional regulator	212954-214102
			<i>mecI</i>	214575-214946
			<i>mecR1</i>	214946-216703
			<i>mecA</i>	216803-218809
			<i>maoC</i>	218855-219283
			<i>ugpQ</i>	219380-220123
			<i>hmg-coA</i>	221040-221207
			Mobile element protein	221465-222139
			Hypothetical protein 3: 100% FN433596 (SCCmec III – J3)	222271-222513
M1640 (S. sciuri)	SCCmec III-like structure A (62689)	TTAATGATGCGGTTTT	CadD	41887-42516
			Hypothetical protein 1: 96.4% AB505630 (SCCmec X-J1)	43277-43942
			putative peptidase	43964-44647
			putative transcriptional regulator	44725-45072
			putative glycosyltransferase	45581-47197
			putative surface protein	47339-50968
			Hypothetical protein 2: 98.48% CP006838 (SCCmec III-J1)	52344-53393
			Hypothetical protein 3: 90.57% CP006838 (SCCmec III-J1)	53497-53814

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			Hypothetical protein 4: 100% CP006838 (SCCmec III-J1)	53814-55601
			ORF	55628-55966
			<i>ccrA3</i>	56141-57505
			<i>ccrB5</i>	57526-59154
			ORF	59625-59975
			Hypothetical protein 5: 78.79% CP006838 (SCCmec III-J2)	59976-60371
			Hypothetical protein 6: 100% CP006838 (SCCmec III-J2)	60390-60911
			Hypothetical protein 7: 43.85% CP006838 (SCCmec III-J2)	61084-61428
			Tnp	61630-63522
			tnp for Tn554	63529-63906
			<i>cadC</i>	64144-64509
			<i>cadA</i>	64493-66916
			CadD	66955-67614
			Hypothetical protein 8: 38.18% CP006838 (SCCmec III-J2)	67832-68353
			Rhodanese-domain containing protein	68922-69986
			B-lactamase domain containing protein	70019-70957
			Hypothetical protein 8: 100% CP006838 (SCCmec III-J1)	71048-71353
			<i>mecR2</i>	71467-72615
			<i>mecI</i>	73088-73459
			<i>mecR1</i>	73459-75198
			<i>mecA</i>	75313-77322
			Hypothetical protein 9: 42.40% AB872255 (SCCmec IV-J3)	77315-77698
			<i>ugpQ</i>	77893-78636
			Tnp	79978-80652
			Hypothetical protein 10: 96.32% AB872255 (SCCmec IV-J3)	81338-82642
K116 (S. sciuri)	SCC _{K116} (35661)	AGTTTTATTTGTGATATGCTT	Photolyase-truncated	17118-17730
			ABC transporter permease	18548-19597
			ORF	19609-20224
			General stress protein 26	21135-21428
			Dehydrosqualene desaturase	21480-22985

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			Dehydrosqualene synthase	22982-23863
			Glycosyltransferase	23919-24962
			Oxidase	25023-26519
			Acyltransferase precursor	26520-26993
			ORF	26998-27498
			ORF	28140-29534
			<i>adhC</i> /alcohol dehydrogenase	30512-31663
			ORF	31845-32360
			Threonine dehydrogenase	32544-33581
			<i>chrA</i>	33690-34852
			<i>Tnp</i>	36633-37496
			<i>Tnp</i>	37460-38011
			<i>cadX</i>	38208-38630
			<i>cadD</i>	38648-39265
			NAD dependent epimerase/dehydrogenase	40058-40495
			NAD dependent epimerase	40479-40724
			Hypothetical protein 1: 91.19% CP006838 (SCCmec III-J2)	41545-42057
			Hypothetical protein 2: 98.08% CP006838 (SCCmec III-J2)	42077-42388
			Hypothetical protein 3: 89.74% JQ412578 (SCCmec II-J2)	42473-42823
			75% <i>ccrC</i>	42928-44604
			Hypothetical protein 4: 79.68% AB781449 (SCCmec V-J2)	44830-46473
			Hypothetical protein 5: 73.17% AB781449 (SCCmec V-J2)	46473-46841
SS27 (SCC-CI_{SS27}) (<i>S. sciuri</i>)	SCC _{SS27 I} (41603)	TATCATAAATGATGCGGTTTTTT	Type II methyltransferase	907-1737
			ORF	1724-4489
			ORF	4673-5038
			Hypothetical protein 1: 77.02% CP006838 (SCCmec III-J2)	5097-5492
			Hypothetical protein 2: 89.95% AB505630 (SCCmec X-J2)	5493-5846
			<i>ccrB3</i>	6318-7946
			<i>ccrA1</i>	7967-9319

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			ORF	9875-11713
			ORF	12103-13641
			<i>rep</i>	13751-14914
			ORF	14928-15722
			Transmembrane protein	16119-16874
			ORF	16147-16542
			Rhodanese-domain containing protein	17272-18339
			Metallo- β lactamase family protein	18368-19702
			DNA-invertase	19873-20454
			<i>Tnp</i>	20710-21879
			ATP-binding domain	21872-22687
			<i>sin</i> recombinase	22821-23426
			ORF	23487-23831
			Copper ATPase	24325-26430
			Multicopper oxidase	26445-27878
			Lipoprotein ACME	27898-28440
			<i>cadD</i>	28933-29547
			<i>Tnp</i>	29658-30461
			<i>cadA</i>	30877-33294
			<i>cadC</i>	33287-33655
			Arsenate reductase	34295-34690
			Arsenic efflux pump protein	34708-36000
			ArsR	36000-36314
			Putative dehydrogenase	36311-37975
			Arsenical pump-driving ATPase	37975-39738
			Trans regulator of arsenic operon	39704-40093
			Arsenical resistance repressor	40572-40892
			Putative membrane protein	40975-41862
SS27 (SCC-CI _{SS27}) (<i>S. sciuri</i>)	SCC _{SS27 II} (15334)	AAAACCGCATCACTATATGATAAGC	ORF	42715-44439

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			ORF	44510-45121
			ORF	45150-46352
			Hypothetical protein 1: 73.14% AB505628 (SCCmec IX-J2)	46433-46954
			Hypothetical protein 2: 97.47% AB505628 (SCCmec IX-J2)	46972-47367
			Hypothetical protein 3: 94.07% CP002120 (SCCmec II-J2)	47368-47721
			<i>ccrB3</i>	48187-49818
			<i>ccrA1</i>	49839-51188
			Hypothetical protein 4: 76.9% AB705452 (SCCmec IX-J1)	51380-51721
			Hypothetical protein 5: 73.14% LK02544 (SCCmec XI-J1)	51724-53538
			Hypothetical protein 6: 61.81% AB097677 (SCCmec IV-J2)	53949-55019
			Hypothetical protein 7: 79.28% AB097677 (SCCmec IV-J2)	55019-56548
			ORF	56548-57501
402567 (S. fleurettii)	SCC ₄₀₂₅₆₇ (17929)	AAAAAACCGACTCATTATGT	ORF	4731-6800
			ORF	6801-8126
			ORF	7420-7740
			ORF	8263-10338
			ORF	10968-12395
			Hypothetical protein 1: 75% AB705452(SCCmec IX-J2)	12521-14311
			ORF	12976-13287
			<i>ccrA</i> new type 2: 77% <i>ccrA1</i>	14793-16160
			<i>ccrB5</i>	16180-17808
			Hypothetical protein 2: 96% CP005288 (SCCmec III-J2)	18279-18629
			Hypothetical protein 3: 77.53% CP005288 (SCCmec III-J2)	18630-19025
			ORF	19041-19547
			ORF	20460-21422
			ORF	21454-22404
401946 (S. vitulinus)	SCC ₄₀₁₉₄₆ (32443)	AAAAAACCGCATCATT	ORF	446-1519
			Type I restriction/modification system	4045-5676
			ORF	5661-6221
			ORF	6230-7261

Strain (species)	Element (bp)	Direct repeats (DR) or inverse repeats (IR)	Gene/protein*	Position in contig
			ORF	7194-8234
			ORF	8235-8795
			Hypothetical protein 1: 51.26% HF569109 (SCCmec IV-J3)	8780-10462
			Type I restriction/modification system DNA methyltransferase subunit M	15060-16514
			Type I restriction/modification system DNA methyltransferase subunit S	16504-17763
			<i>hsdR</i>	17741-20869
			ORF	21448-21954
			ORF	21970-22287
			<i>ccrB</i> new type 1: 76% <i>ccrB1</i>	23189-24829
			<i>ccrA</i> new type 1: 82% <i>ccrA1</i>	24838-26187
			Hypothetical protein 2: 75.86% AB063173 (SCCmec IX-J1)	26690-28480
			Hypothetical protein 3: 81.89% KM369884 (SCCmec V-J1)	31355-32257
CH10 (<i>S. vitulinus</i>)	SCC _{CH10} (11684)	ATTATTAGATTTTTT	ORF	243-2318
			Hypothetical protein 1: 97.20% AB705452 (SCCmec IX-J2)	2949-4376
			Hypothetical protein 2: 95.20% AB705453 (SCCmec IX-J1)	4502-6292
			<i>ccrA</i> new type 2: 82.74% <i>ccrA3</i>	6465-7832
			<i>ccrB</i> new type 4: 81% <i>ccrB4</i>	7852-9486
			Hypothetical protein 3: 89.97% AB705452 (SCCmec IX-J1)	9960-10298
			Hypothetical protein 4: 83.33% AB705452 (SCCmec IX-J1)	10394-10705
			Hypothetical protein 5: 56.61% AB705452 (SCCmec IX-J1)	10721-11233
			ORF	11615-12034
			ORF	12485-13579
			ORF	13621-15297

* when the gene is not identified, only the most similar protein present in the NCBI database is shown.

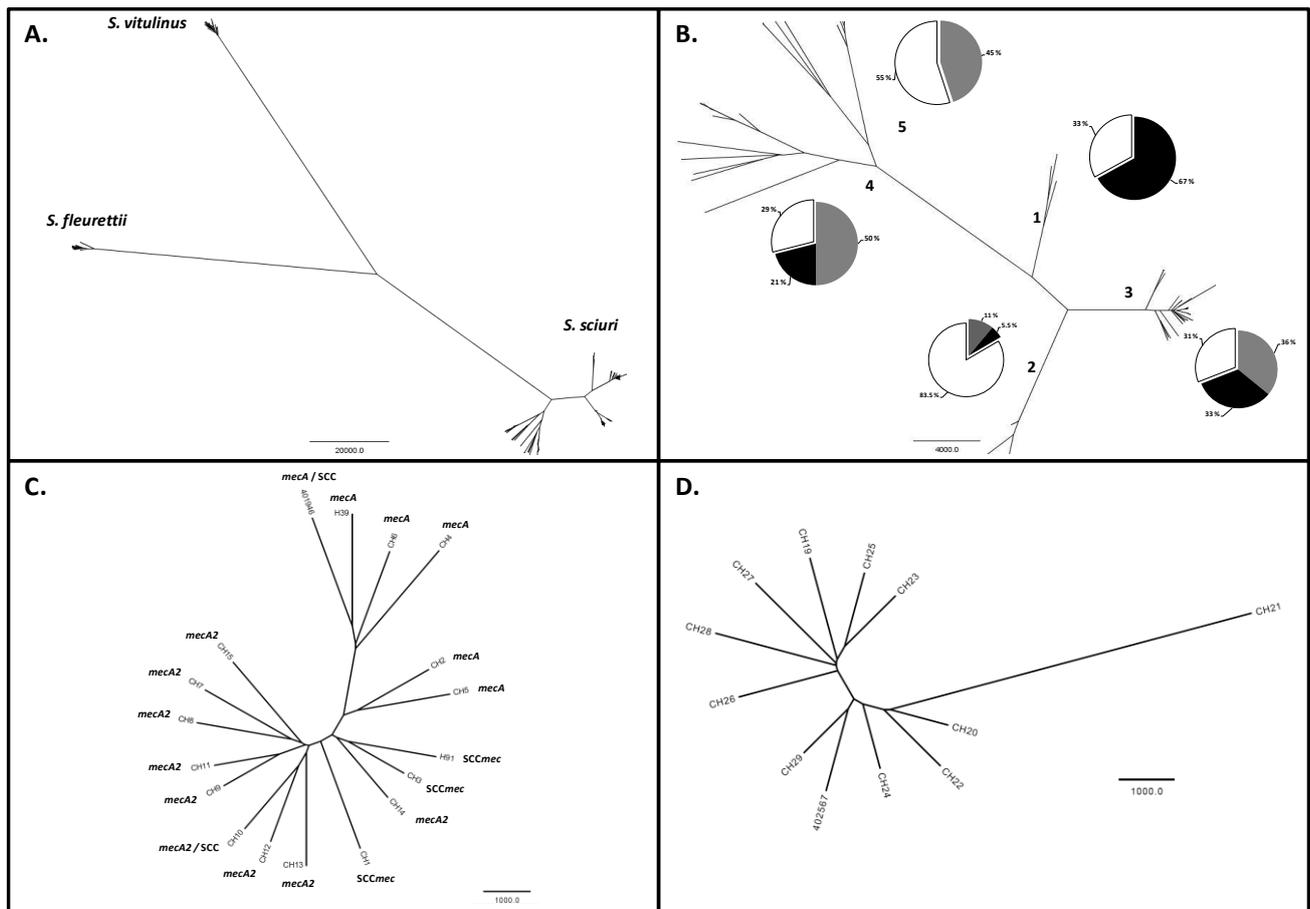
Supplementary Table S3. Predicted ORFs of the *orfX*-containing contig of *ccr*-negative strain K22. Nucleotide sequences of the predicted ORFs were compared with the ones available at <http://www.ncbi.nlm.nih.gov/>.

Position in contig	Gene *	Species *
10..846	Similar to MCCL_1950/ <i>parB</i>	<i>M. caseolyticus</i>
1415..2521	Similar to A284_11420/cystathione gamma synthase	<i>S. warneri</i>
2518..3690	Similar to SERP0036/trans-sulfuration enzyme	<i>S. epidermidis</i>
3647..5485	Similar to SSP2415/methyltransferase	<i>S. saprophyticus</i>
5482..7728	Similar to SAMSHR1132_03290/methyltransferase	<i>S. aureus</i>
7745..8488	Similar to A284_11440/metal dependent hydrolase	<i>S. warneri</i>
8602..10056	Similar to SSP2440/ <i>cstA</i>	<i>Bacillus sp."</i>
10208..11071	Similar to MCCL_1952/ <i>ParB</i> protein homologue	<i>M. caseolyticus</i>
11088..11807	<i>gidB</i>	<i>M. caseolyticus</i>
11809..13683	<i>gidA</i>	<i>S. pasteurii</i>
13699..15078	Similar to SAEMRSA15_26100/tRNA modification GTPase	<i>S. aureus</i>
15192..15989	Similar to MCCL_1956/single stranded DNA binding protein	<i>M. caseolyticus</i>
16019..16369	Similar to <i>rnpA</i> /ribonuclease protein component	<i>S. epidermidis</i>
16461..16598	Similar to SPSINT_0001/ribosomal protein	<i>S. pseudointermedius</i>
17150..18490	<i>dnaA</i>	<i>S. haemolyticus</i>
18657..19790	<i>dnaN</i>	<i>S. carnosus</i>
20152..21051	Similar to MCCL_0003/ <i>Na</i> efflux pump	<i>M. caseolyticus</i>
24025..24246	Similar to X998_0003/S4 domain protein	<i>S. aureus</i>
24250..25365	<i>recF</i>	<i>S. haemolyticus</i>
25388..27310	<i>gyrB</i>	<i>S. warneri</i>
27344..29944	Similar to A284_00030/DNA gyrase	<i>S. warneri</i>
30018..30614	Similar to SH0007/ <i>hyp</i> core protein	<i>S. haemolyticus</i>
31050..31487	<i>hutP</i>	<i>Bacillus sp."</i>
31582..33066	Similar to STP1_1390/histidina ammonia lyase	<i>S. pasteurii</i>
33094..34404	Similar to SCA_1829/ <i>hyp</i> core protein	<i>S. carnosus</i>
34422..36089	Similar to <i>hutU</i> /urocanate hydratase"	<i>S. carnosus</i>
36082..37323	Similar to STP1_0815/imidazolepropionase	<i>S. pasteurii</i>
37631..38908	Similar to SAMSHR1132_00090/seryl tRNA synthase	<i>S. aureus</i>
39033..39548	Similar to CH52_05575/ <i>hyp</i> core protein	<i>S. aureus</i>
39824..40468	Similar to SAMSHR1132_00100/membrane protein	<i>S. aureus</i>
41027..41998	Similar to SERP2541/homoserine-o-acetyltransferase	<i>S. epidermidis</i>
43012..44976	Similar to STP1_1384/DHHA1 domain containing protein	<i>S. pasteurii</i>
45513..46922	Similar to CH52_05370/DNA helicase	<i>S. aureus</i>
47209..48495	<i>purA</i>	<i>S. aureus</i>
49483..50367	Similar to MCCL_0020/ <i>hyp</i> core protein	<i>M. caseolyticus</i>

Position in contig	Gene *	Species *
50808..51509	Two-component response regulator	<i>S. sciuri</i>
51519..53360	Two-component sensor kinase	<i>S. sciuri</i>
53335..54675	<i>yycH</i>	<i>S. sciuri</i>
54675..55466	hypothetical protein SA_21	<i>S. sciuri</i>
55498..56289	Zn-dependent hydrolase	<i>S. sciuri</i>
56584..5706	<i>orfX</i>	<i>S. sciuri</i>
57138..58442	Similar to SAKOR_01992/potassium uptake protein	<i>S. aureus</i>
58611..58955	<i>arsC</i>	<i>S. sciuri</i>
59027..60316	<i>arsB</i>	<i>S. sciuri</i>
60845..63874	putative phage infection protein	<i>S. sciuri</i>
64173..65006	Similar to SERP2401/serine protease	<i>S. epidermidis</i>
70703..72076	Similar to deoxyribodipyrimidine photolyase"	<i>S. xylosus</i>
72122..72541	hyp core protein <i>S. xylosus</i>	<i>S. xylosus</i>
72701..73741	putative alcohol dehydrogenase	<i>S. sciuri</i>
74151..75131	<i>dus</i> /tRNA synthase	<i>S. aureus</i>
75352..76749	Similar to SCA_2443/hyp core protein	<i>S. carnosus</i>
77115..78032	Similar to SAMSHR1132_20200/putative exported protein	<i>S. aureus</i>
78488..79813	Similar to SPSINT_2422/hyp core protein	<i>S. pseudointermedius</i>
80071..83217	Similar to SSP0074/hyp core protein	<i>S. saprophyticus</i>
84623..86254	<i>xyB</i> /xylulokinase	<i>S. carnosus</i>
86223..86918	Similar to M7W_2352/epimerase	<i>E. faecium</i>
86932..88353	Similar to araA2/arabinose isomerase	<i>E. faecium</i>
88409..89815	Similar to T256_00940/sugar transporter	<i>Pediococcus sp.</i>
89882..90736	<i>blaZ</i>	<i>S. aureus</i>
90874..91191	Similar to SCA_2438/hyp core protein	<i>S. carnosus</i>
91286..92236	Similar to SSP1638/putative lipase	<i>S. saprophyticus</i>
92431..93354	Similar to SCA_2436/hyp core protein	<i>S. carnosus</i>
93356..94051	Similar to SCA_2435/hyp core protein	<i>S. aureus</i>
94280..95605	Similar to SSP0521/hyp core protein	<i>S. saprophyticus</i>
95602..96618	Similar to SSP0520/putative oxidoreductase	<i>S. saprophyticus</i>
96960..97487	Similar to SAMSHR1132_22300/acetyltransferase	<i>S. aureus</i>
97503..98294	Similar to lin2443/ABC transporter	<i>Listeria sp.</i>
98313..99026	Similar to LMOSLCC2376_2243/ABC transporter/permease	<i>Listeria sp.</i>
99038..99742	Similar to AX10_05710/cysteine ABC transporter/permease	<i>Listeria sp.</i>
99743..100525	Similar to <i>yecC</i> /ATP transporter permease ATP binding protein	<i>Listeria sp.</i>
100720..101481	Similar to SSP2181/transcriptional regulator	<i>S. saprophyticus</i>
101546..102784	Similar to SSP2180/alpha-ketoglutarate permease	<i>S. saprophyticus</i>
102808..103878	Similar to A284_10560/dehydrogenase	<i>S. warneri</i>
104040..105671	Similar to A284_10555/ribulokinase	<i>S. warneri</i>
105831..106085	Similar to STP1_1355/prevent host death protein	<i>S. pasteurii</i>
106900..107373	Similar to MC28_F090/acetyltransferase	<i>Bacillus sp</i>

Position in contig	Gene *	Species *
112374..113495	FAD-dependent oxidoreductase	<i>S. haemolyticus</i>
113489..114829	<i>feoB</i> +putative membrane protein	<i>S. haemolyticus</i>
115380..116267	SERP2386/colabamin synthesis protein	<i>S. epidermidis</i>
116528..117478	SPSINT_2071/uroporphyrinogen methyltransferase	<i>S. pseudointermedius</i>
117469..117786	<i>nirD</i>	<i>S. pseudointermedius</i>
117789..120194	SPSINT_2073/nitrite reductase	<i>S. pseudointermedius</i>
121609..123039	Similar to Pcryo_0766/dicarboxylate anaerobic carried	<i>Psychrobacter sp.</i>
124183..126057	Similar to Cbei_0699/phosphotransferase	<i>Clostridium sp.</i>
126054..127472	Similar to Cbei_0700/glycoside hydrolase	<i>Clostridium sp.</i>
127687..128667	Similar to STP1_1330/alpha-β family hydrolase	<i>S. pasteurii</i>
128682..129251	Similar to STP1_1331/acetyltransferase	<i>S. pasteurii</i>
129372..130241	Similar to STP1_1332/LysR transcriptional regulator	<i>S. pasteurii</i>
130979..132601	Similar to SCA_2062/hyp core protein	<i>S. carnosus</i>
132890..134380	Similar to SCA_2061/allantoin permease	<i>S. carnosus</i>
134370..135731	Allantoinase	<i>S. xylosum</i>

* nucleotide sequences with the highest BLAST score; hyp: hypothetical



Supplementary Figure 1. Phylogenetic tree reflecting the number of SNP differences among the genomes of the isolates studied. *S. fleurettii* 402567 was used as a reference. **A.** All genomes (*S. sciuri*, *S. fleurettii*, *S. vitulinus*). **B.** *S. sciuri* genomes. Phylogenetic groups were defined according with the number of single-nucleotide polymorphisms (SNPs) differences. Phylogenetic group 1: new subspecies group 1; phylogenetic group 2: *S. sciuri sciuri*; phylogenetic group 3: new subspecies group 3; phylogenetic group 4: *S. sciuri rodentius*; phylogenetic group 5: *S. sciuri carnaticus*. The distribution of SCCmec and SCC elements among the isolates belonging to each phylogenetic group (1-5) is also shown; black: SCCmec; grey: SCC; white: no carriage of SCCmec/SCC. **C.** *S. vitulinus* genomes. The distribution of *mec* homologues, SCC and SCCmec elements is shown. **D.** *S. fleurettii* genomes.

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